

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: March 1, 2001, 16:09:34 ; Search time 299.73 seconds  
(without alignments)  
16.424 Million cell updates/sec

Title: US-09-331-631A-8\_COPY\_120\_161  
Perfect score: 245 SQRFQECQHQHQEQRPE.....QQCVREREKQYENPWRGE 42  
Sequence: BIOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700  
Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_15:\*

1: sp\_archaea:\*

2: sp\_bacteria:\*

3: sp\_fungi:\*

4: sp\_human:\*

5: sp\_invertebrate:\*

6: sp\_mammal:\*

7: sp\_mhc:\*

8: sp\_organelle:\*

9: sp\_phage:\*

10: sp\_plant:\*

11: sp\_rodent:\*

12: sp\_virus:\*

13: sp\_vertebrate:\*

14: sp\_uniclassified:\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES					
Result No.	Score	Query Match	Length	DB ID	Description
1	111.5	45.5	525	10 Q43358	043358 theobroma cacao
2	103	42.0	593	10 Q9EW4 Juglans regia	Q9EW4 juglans regia
3	99	40.4	625	10 Q9EW4 Juglans regia	Q9EW4 juglans regia
4	98	40.0	666	10 Q9SP1 Juglans regia	Q9SP1 juglans regia
5	94	38.4	666	10 Q9SP1 Juglans regia	Q9SP1 juglans regia
6	91	37.1	393	10 Q9ZP0 Oryza sativa	Q9ZP0 oryza sativa
7	74	30.2	900	5 Q9VK9 Drosophila melanogaster	Q9VK9 drosophila melanogaster
8	74	30.2	3828	5 Q24J42 Drosophila melanogaster	Q24J42 drosophila melanogaster
9	72	29.6	402	10 Q9ZR8 Oryza sativa	Q9ZR8 oryza sativa
10	72	29.4	425	5 Q17H0 Juglans regia	Q17H0 juglans regia
11	72	29.4	600	5 Q17401 Caenorhabditis elegans	Q17401 caenorhabditis elegans
12	70	28.6	637	10 Q03678 Oryza sativa	Q03678 oryza sativa
13	70	28.6	905	5 Q18260 Caenorhabditis elegans	Q18260 caenorhabditis elegans
14	69.5	28.4	328	5 Q9VE66 Drosophila melanogaster	Q9VE66 drosophila melanogaster
15	69	28.2	925	5 Q9Y7C5 Drosophila melanogaster	Q9Y7C5 drosophila melanogaster
16	69	28.2	2123	5 Q0U9S7 Drosophila melanogaster	Q0U9S7 drosophila melanogaster
17	68	27.8	57	4 Q9YAJ1 Homo sapiens	Q9YAJ1 homo sapiens
18	68	27.8	930	5 Q9SY9 Drosophila melanogaster	Q9SY9 drosophila melanogaster
19	67.5	27.6	709	5 Q9NMR2 Caenorhabditis elegans	Q9NMR2 caenorhabditis elegans

ALIGMENTS

RESULT	PRELIMINARY:	PRT;	525 AA.
043358	043358		
ID	ID		
AC	AC		
DT	DT	01-NOV-1995 (TREMBLrel. 01; Created)	
DT	DT	01-OCT-2000 (TREMBLrel. 01; Last sequence update)	
DE	DE	VICILIN PRECURSOR.	
GN	GN	CSV.	
OS	OS	Theobroma cacao (Cacao).	
OC	OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Eudicots; Rosidae; Malvales; Malvaceae; Theobroma.	
OC	OC	Malvales; Malvaceae; Theobroma.	
OX	OX	NCBI_Tax ID:3641;	
RN	RN	[1]	
RP	RP	SEQUENCE FROM N.A.	
RC	RC	TISSUE=LEAVES;	
RX	RX	MEDLINE=92288309; PubMed=1600151;	
RA	RA	McHenry L., Fritz P.J.;	
RT	RT	*Comparison of the structure and nucleotide sequences of vicilin genes of cocoa and cotton raise questions about vicilin evolution.;	
RT	RT	Plant Mol. Biol. 18:1173-1176(1992).	
RL	RL	MENDL; 31919; Thecc:1188;30919.	
DR	DR	X62656; CAA44949.1; -.	
EMBL	EMBL	X62656; CAA44949.1; -.	
DR	DR	INSP; P02453; PHBL.	
DR	DR	MENDL; 31919; Thecc:1188;30919.	
DR	DR	INTERPRO; IPR001113; -.	
PFAM	PFAM	PF00546; Seedscore_7s; 1.	
DR	DR	PRODOM; P0081059; -; 1.	
KW	KW	Signal.	
FT	FT	SIGNAL 1 24 POTENTIAL.	
FT	FT	CHAIN 25 VICILIN	
FT	FT	SEQUENCE 525 AA; 60798 MW; 19114CD5C248905D CRC64;	

Query Match Best Local Similarity 45.5%; Score 111.5; DB 10; Length 525; Matches 20; Conservancy 9; Mismatches 10; Indels 1; Gaps 1

QY 2 OROFOCQHQHQEPRKEQQCVCRCREKQYENPWRGE 41

Db 82 QROQOCQGRQEQQGOREQQCORKWEQKEQ3-RGE 120

RESULT 2

ID Q9SEW4 PRELIMINARY; PRT; 593 AA.

AC Q9SEW4;

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-OCT-2000 (TREMBLrel. 13, Last annotation update)

DE VICTILIN-LIKE PROTEIN PRECURSOR (FRAGMENT).

OS Juglans regia (English walnut).

OC Bukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots; Rosidae; eurossids I; Fagales; Juglandaceae; Juglans.

OC NCBI\_TaxID=51240;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CV SUNLAND; TISSUE=SONAMIC EMBRYO LINE;

RA Teuber S.S., Jarvis K.C., Peterson W.R., Dandekar A.M., Ansari A.A.;

RT "Identification and cloning of a cDNA encoding a vicilin-like protein, Jug r 2, from English walnut kernel (Juglans regia): a major food allergen.";

RT Submitted (MAY-1998) to the EMBL/genBank/DBJ databases.

DR EMBL; AF06055; AAF18269.1; -.

DR HSSP; P02853; 2PHL.

DR INTERPRO; IPR001113; -.

DR PFAM; PF00546; Seedstore\_7s; 1.

FT NON\_TER 1 1

SQ SEQUENCE 593 AA; 69990 MW; 9BA127E19B18C0D8 CRC64;

Query Match 42.0%; Score 103; DB 10; Length 593; Best Local Similarity 42.1%; Pred. No. 8e-05; Matches 16; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

Qy 2 OROFOECQQHQHQQPERKEKKQQVRECREKQYQINPWR 39

Db 120 QQYHRCQRCQTOHQSPERORQCQRCEROYKBCQGR.157

RESULT 3

ID Q9SPJ3 PRELIMINARY; PRT; 625 AA.

AC Q9SPJ3;

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-OCT-2000 (TREMBLrel. 13, Last sequence update)

DE VICTILIN PRECURSOR (FRAGMENT).

GN AMP2.

OS Macadamia integrifolia (Macadamia nut).

OC Eukaryota; Viridiplantae; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; Proteaceae; Macadamia.

OX NCBI\_TaxID=60598;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=NUT KERNEL;

RA Marcus J.P., Goulter K.C., Green J.L., Manners J.M.;

RT "A family of antimicrobial peptides is produced by processing of a 7S globulin protein in Macadamia integrifolia.";

RL Plant J. 0:0-0(1999).

DR EMBL; AF161883; ARD54246.1; -.

DR HSSP; P02853; 2PHL.

DR INTERPRO; IPR001113; -.

DR PFAM; PF00546; Seedstore\_7s; 1.

FT NON\_TER 1 1

SQ SEQUENCE 625 AA; 7356 MW; 415808A89D370296 CRC64;

Query Match 40.4%; Score 99; DB 10; Length 625; Best Local Similarity 38.3%; Pred. No. 0.00025; Matches 18; Conservative 11; Mismatches 8; Indels 10; Gaps 2;

Qy 2 QROFECQQHQHQQPERKEKKQQVRECREKQYQE-----NPWRG 40

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RESULT 4

ID Q9SPJ4 PRELIMINARY; PRT; 666 AA.

AC Q9SPJ4;

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-OCT-2000 (TREMBLrel. 13, Last sequence update)

DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)

DE VICTILIN PRECURSOR.

GN AMP2.

RC Macadamia integrifolia (Macadamia nut).

RA Eukaryota; Viridiplantae; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; Proteaceae; Macadamia.

OX NCBI\_TaxID=60598;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=NUT KERNEL;

RA Marcus J.P., Goulter K.C., Green J.L., Manners J.M.;

RT "A family of antimicrobial peptides is produced by processing of a 7S globulin protein in Macadamia integrifolia.";

RL Plant J. 0:0-0(1999).

DR EMBL; AF161883; ARD54245.1; -.

DR HSSP; P02853; 2PHL.

DR INTERPRO; IPR001113; -.

DR PFAM; PF00546; Seedstore\_7s; 1.

DR SEQUENCE 666 AA; 78217 MW; 0ECA22F8710F8A7B CRC64;

Query Match 38.4%; Score 94; DB 10; Length 666; Best Local Similarity 35.3%; Pred. No. 0.0011; Matches 12; Conservative 11; Mismatches 11; Indels 0; Gaps 0;

Qy 2 QROFECQQHQHQQPERKEKKQQVRECREKQYQE-----NPWRG 40

Db	123 QQQYEQCOKHCORRETEPRHMOTCQQRGERRYEK	156
RESULT	6	
ID	Q9ZTP0	PRELIMINARY; PRT; 393 AA.
AC	Q9ZTP0;	
DT	01-MAY-1999 (TREMBLrel. 10, Created)	
DT	01-MAY-1999 (TREMBLrel. 10, Last sequence update)	
DT	01-MAY-1999 (TREMBLrel. 10, Last annotation update)	
DE	HYPOTHETICAL 45.3 KDa PROTEIN.	
GN	OSB705.	
OS	Oryza sativa (Rice).	
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;	
OC	Magnoliophyta; Liliopsida; Poales; Poaceae; Oryza.	
OX	NCBI_TaxID=4530;	
[1]	SEQUENCE FROM N.A.	
RC	STRAIN=LAMELLO;	
RA	Chen, W., Chen, L.J.;	
RL	Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.	
DR	EMBL: AF049348; AAD02494.1; -.	
KW	Hypothetical protein.	
SQ	SEQUENCE 393 AA; 45258 MW; DBD01934BA2F9E95 CRC64;	
RESULT	7	
ID	Q9VK09	PRELIMINARY; PRT; 900 AA.
AC	Q9VK09;	
DT	01-MAY-2000 (TREMBLrel. 13, Created)	
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)	
DT	01-JUN-2000 (TREMBLrel. 14, Last annotation update)	
DE	CG6043 PROTEIN.	
GN	CG6043.	
OS	Drosophila melanogaster (Fruit fly).	
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;	
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;	
OC	Ephydriidae; Drosophilidae; Drosophila.	
OX	NCBI_TaxID=7227;	
RN	[1]	SEQUENCE FROM N.A.
RP	SEQUENCE FROM N.A.	
RC	STRAIN=BERKELEY;	
RX	Medline:20196006; PubMed=10731132;	
RA	Adams, M.D., Celrniker, S.E., Holt, R.A., Evans, C.A., Gocayne, J.D.,	
RA	Amanatides, P.G., Scherer, S.E., Li, P.W., Hoskins, R.A., Galle, R.F.,	
RA	George, R.A., Lewis, S.E., Richards, S., Astbury, M., Hendeisen, S.N.,	
RA	Sutton, G.G., Wortman, J.R., Yandell, M.D., Zhang, Q., Chen, L.X.,	
RA	Brandon, R.C., Rogers, Y.-H.C., Blazej, R.G., Champe, M., Pfeiffer, B.D.,	
RA	Wan, K.H., Doyle, C., Baxter, G., Heit, G., Nelson, C.R., Miklos, G.L.G.,	
RA	Abril, J.F., Agbayani, A., An, H.-J., Andrews-Pfannkoch, C., Baldwin, D.,	
RA	Ballew, R.M., Basu, A., Baxendale, J., Bayraktaroglu, L., Beasley, E.M.,	
RA	Beeson, K.Y., Benos, P.V., Berman, B.P., Brandari, D., Bolshakov, S.,	
RA	Borkov, D., Botchan, M.R., Bouck, J., Broestlein, P., Brotchie, P.,	
RA	Burtis, K.C., Busam, D.A., Butler, H., Cadieu, E., Centter, A., Chandra, I.,	
RA	Cherry, J.M., Cawley, S., Dahlke, C., Davenport, L.B., Davies, P.,	
RA	de Pablo, B., Delcher, A., Deng, Z., Mays, A.D., Dew, I., Dietz, S.M.,	
RA	Dobson, K., Doup, L.E., Downes, M., Dugan-Rocha, S., Dunckov, B.C., Dunn, P.,	
RA	Fosler, C., Evangelista, C.C., Ferreria, S., Fleischmann, W.,	
RA	Gebel, A.E., Garg, N.S., Gelbart, W.M., Glasser, K., Glodek, A., Gong, F., Gorrell, J.H., Gu, Z., Guan, P., Harris, M.,	
RA	Harris, N.L., Harvey, D., Heiman, T.J., Hernandez, J.R., Houck, J.,	
RA	Hostin, D., Houston, K.A., Howland, T.J., Wei, M.-H., Ibegwam, C., Jalali, M., Kalush, F., Karpen, G.H., Ke, Z., Kennison, J.A., Ketchum, K.A.,	
RA	Kimmel, B.E., Koide, C.D., Kraft, C., Kravitz, S., Kulp, D., Lai, Z.,	
RA	Lasko, P., Lei, Y., Levitsky, A.A., Li, J., Li, Z., Liang, Y., Lin, X.,	
RA	Liu, X., Mattei, B., McIntosh, T.C., McLeod, M.P., McPherson, D.,	
RA	Merkulov, G., Mishina, N.V., Mobarry, C., Morris, J., Mostafavi, A.,	
RA	Mouton, S.M., Moy, M., Murphy, L., Muzny, D.M., Nelson, D.L.,	
RA	Nelson, D.R., Nelson, K.A., Nixon, K., Nusskern, D.R., Pacieba, J.M.,	
RA	Palazzolo, M., Pittman, G.S., Pan, S., Pollard, J., Puri, V., Reese, M.G.,	
RA	Reinert, K., Remington, K., Saunders, R.D.C., Scheeler, F., Shen, H.,	
RA	Shue, B.C., Sideris-Kiamos, I., Simpson, M., Skupski, M.P., Smith, T.,	
RA	Spier, E., Spradling, A.C., Stapleton, M., Strong, R., Sun, E.,	
RA	Svirskas, R., Tector, C., Turner, R., Venter, E., Wang, A.H., Wang, X.,	
RA	Wang, Z.-Y., Wasserman, D.A., Weinstock, G.M., Weissenbach, J.,	
RA	Williams, S.M., Woodage, T., Worley, K.C., Wu, D., Yang, S., Yao, Q.A.,	
RA	Ye, J., Yeh, R.-F., Zaveri, J.S., Zhan, M., Zhang, G., Zhao, Q., Zheng, L.,	
RA	Zheng, X.H., Zhong, F.N., Zong, W., Zhou, X., Zhu, S., Zhu, X., Smith, H.O.,	
RA	Gibbs, R.A., Myers, E.W., Rubin, G.M., Venter, J.C.,	
RT	"The genome sequence of <i>Drosophila melanogaster</i> ."	
RL	Science 287:2183-2195 (2000).	
DR	EMBL: AE003639; AAC53274.1; -.	
DR	FLYBASE: FBgn0032497; CG6043.	
DR	INTERPRO: IPR002965; -.	
DR	PRINTS: PRO1217; PRICHEXTENSN.	
SEQUENCE	900 AA; 98948 MW; DD99C0057/CDAS5E44 CRC64;	
RESULT	8	
ID	Q24742	PRELIMINARY; PRT; 3828 AA.
AC	Q24742;	
DT	01-NOV-1996 (TREMBLrel. 01, Created)	
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)	
DT	01-OCT-2000 (TREMBLrel. 15, Last annotation update)	
DE	PREDICTED TRITHORAX PROTEIN.	
OS	Drosophila virilis (Fruit fly).	
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;	
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;	
OC	Ephydriidae; Drosophilidae; Drosophila.	
OX	NCBI_TaxID=7244;	
RN	[1]	SEQUENCE FROM N.A.
RP	Tillio, S., Sedkov, Y., Mizrokh, L., Mazo, A.;	
RL	Mech. Dev. 0:0-0 (1995);	
DR	EMBL: Z50038; CA09349.1; -.	
DR	HSPP; P19793; 2NLL.	
DR	FLYBASE: FBgn0014844; Dvirl\trx.	
DR	INTERPRO: IPR001214; -.	
DR	INTERPRO: IPR001965; -.	
DR	PFAM: PF00028; PHD; 2.	
DR	PFAM: PF00856; SET; 1.	
SEQUENCE	3828 AA; 413721 MW; 32059CP303A3C504 CRC64;	
Query Match	30.2%	Score 74; DB 5; Length 3828;
Best Local Similarity	38.2%	Pred. No. 1.3; Mismatches 7; Indels 0; Gaps 0;
Matches	13;	Conservative 14; Mismatches 7; Indels 0; Gaps 0;
QY	2	2 QROFORCQHQHQOEPRPEKKQQCVRECREYQE 35
Db	2995	QQEQPQQEQHQHQQQQQQQQQQQQQQQQQQQQQQQ 3028
RESULT	9	
ID	Q9ZRHB	PRELIMINARY; PRT; 402 AA.

AC 09ZRRB;  
DT 01-MAY-1999 (TREMBLrel. 10, Created)  
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
DE EARLY EMBRYOGENESIS PROTEIN.  
GN OSE362.  
OS Oryza sativa (Rice).  
OC Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Oryza.  
OX NCBI\_TaxID=4530;  
[1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CV. TAINUNG 67;  
RA Tseng M.J., Wang C.S., Hsu H.R.;  
RL Submitted (APR 1995) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; U25669; AAD10370.1; -;  
SEQUENCE 402 AA; 44252 MW; F03C86948F840060 CRC64;

Query Match 29.6%; Score 72.5; DB 10; Length 402;  
Best Local Similarity 39.5%; Pred. No. 0.27;  
Matches 15; Conservative 8; Mismatches 6; Indels 9; Gaps 3;

Qy 6 QECQOHC-HQEQERREKKQOCVRECREEKQENPWRGER 42  
Db 252 QOCRKOCOHHDQ-WKKQQCMQDCRQ-----WRRR 281

RESULT 10  
ID 017400 PRELIMINARY; PRT; 425 AA.  
AC 017400;  
DT 01-JAN-1999 (TREMBLrel. 09, Created)  
DT 01-JAN-1999 (TREMBLrel. 09, Last sequence update)  
DE HYPOTHETICAL 45.9 KDA PROTEIN AC3.3 IN CHROMOSOME V PRECURSOR.  
GN AC3.3.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
OC Rhabditida; Nematoda; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
[1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BRISTOL N2;  
RA McMurray A.;  
RL Submitted (APR 1996) to the EMBL/GenBank/DDBJ databases.  
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).  
CC -!- SIMILARITY: BELONGS TO FAMILY UPF.  
DR EMBL; Z71177; CRA94568.1; -;  
DR WORMPP; AC3.4; CE05134.  
DR INTERPRO; IPR001594; -;  
DR PFAM; PF01529; zf-DHIC; 1.  
DR PRODOM; PD003041; -; 1.  
KW Hypothetical protein; Transmembrane.  
FT TRANSMEM 309 329 POTENTIAL.  
FT TRANSMEM 447 467 POTENTIAL.  
FT TRANSMEM 490 510 POTENTIAL.  
FT DOMAIN 6 287 GLN-RICH.  
SEQUENCE 600 AA; 67740 MW; 504A5CE1BA72091B CRC64;

Query Match 29.4%; Score 72; DB 5; Length 600;  
Best Local Similarity 46.4%; Pred. No. 0.44;  
Matches 13; Conservative 7; Mismatches 4; Indels 4; Gaps 1;

Qy 6 QECQOHC-HQEQERREKKQOCVRECREEKQENPWRGER 29  
Db 24 QOCQQQCVCQTOPIQCQPQCQQCVCQQC 51

RESULT 12  
ID 003678 PRELIMINARY; PRT; 637 AA.  
AC 003678;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)  
DE FETAL STORAGE PROTEIN.  
GN BEG1 OR GB1.  
OS Hordeum vulgare (Barley), and Triticum aestivum (Wheat).  
OC Eukaryota; Viridiplantae; Embryophyta; tracheophyta; Spermatophyta;  
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Hordeum.  
OX NCBI\_TaxID=4513; 4565;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=9328798; PubMed=8510647;  
RA Heck G.R., Chamberlain A.C., Ho T.H.D.;  
RT "Barley embryo globulin 1 gene, Beg1: characterization of cDNA,  
RT chromosome mapping and regulation of expression.";  
RL Mol. Gen. Genet. 239:209-219(1993).  
DR EMBL; M64372; AAA32336.1; -;  
DR EMBL; M81119; AAC34269.1; -;  
DR HSSP; P02853; 2PBL.  
DR MENDEL; 8553; HOYU:1188; 8553.  
DR INTERPRO; IPR000901; -;  
DR INTERPRO; IPR001113; -;  
DR PFAM; PF00546; seedstore\_7's; 1.  
DR PROSITE; PS00867; CPSASE\_2; UNKNOWN\_1.  
DR PRODOM; PA081059; -; 1.  
KW Seed storage protein.  
SEQUENCE 637 AA; 72252 MW; F323FF99947C3C CRC64;

Query Match 28.6%; Score 70; DB 10; Length 637;  
Best Local Similarity 30.6%; Pred. No. 0.8;  
Matches 15; Conservative 7; Mismatches 13; Indels 14; Gaps 2;

Qy 6 QECQOHC-HQEQERREKKQOCVRECREEKQENPWRGER 41  
Db 42 QOCVQRQERPR-YSHARCVQECRDQDQHGRHEQEEGRGRGROWHE 89

RESULT 11  
ID 017401 PRELIMINARY; PRT; 600 AA.  
AC 017401;  
DT 01-JAN-1999 (TREMBLrel. 09, Created)  
DT 01-JAN-1999 (TREMBLrel. 09, Last sequence update)  
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)  
DE HYPOTHETICAL 67.7 KDA PROTEIN AC3.4 IN CHROMOSOME V.  
GN AC3.4.

RESULT	13
018260	PRELIMINARY; PRT; 905 AA.
ID	018260; 045638; (REMBLrel. 05, Created)
AC	01-NOV-1998 (REMBLrel. 08, Last sequence update)
DT	01-JAN-1998 (REMBLrel. 05, Created)
DE	ZC101.1 PROTEIN.
GN	CN101.1.
OS	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabdiidae; Peloderinae; Caenorhabditis.
OC	Rhabdiidae; Dirosophilidae; Drosophila.
OX	Diptera; Brachycera; Muscomorpha;
OC	Ephydriidae; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
NCBI TAXID=7227;	
RN	[1]
RP	SEQUENCE FROM N.A.
RC	SISTRIN-BERKELEY;
RX	MEDLINE=20196006; PubMed=10731132;
RA	Adams M.D., Celiker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazquez R.G., Champe M., Pfleiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abrial J.F., Agbaria A., An H.-J., Andrews-Pflanck C., Baldwin D., Ballew R.M., Basu A., Baxendale H., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Burtsis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de Pablo S., Delcher A., Deng Z., Mays A.D., Dew T., Dietz S.M., Dobson K., Douc L.-E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin R., Ainscough R., Anderson K., Baynes C., Berks M., Craston M., Dear S., Du Z., Durbin R., Favello A., Fulton L., Gardiner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L., Jones M., Kershaw J., Kirstein J., Laister N., Latreille P., Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M., Parsons J., Percy C., Rikoff H., Roopra A., Saunders D., Shownkeen R., Smaldon N., Smith A., Sonnhammer E., Straden R., Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R., Watson A., Weinstock L., Wilkinson-Spratt J., Wohldman P.; [2] 2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans.";
RN	Nature 368:32-38(1994).
RA	[3]
RP	SEQUENCE FROM N.A.
RA	Percy C.; Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
EMBL:	Z03395; CAB07705; 1; JOINED.
EMBL:	Z83112; CAB05541; 1; JOINED.
EMBL:	Z03395; CAB05541; 1; JOINED.
EMBL:	HSSP; P01130; IAJJ; INTERPRO; IPR002172; -.
DR	PFAM; PF00057; ldl receptor; 7.
DR	PRIMIS; PR00261; LDLRECEPTOR.
DR	PROSITE; PS01209; LDLRA_1; 5.
DR	PROSITE; PS50066; LDLRA_2; 7.
KW	Glycoprotein.
SQ	SEQUENCE 905 AA; 102299 MW; 77DACE50D1A7BD24 CRC64;
RESULT	14
09VB66	PRELIMINARY; PRT; 328 AA.
ID	09VE66; (REMBLrel. 13,保守性 11; 错配 9; 插入 0; 缺口 0;)
AC	01-MAY-2000 (REMBLrel. 13, Created)
DT	01-MAY-2000 (REMBLrel. 13, Last sequence update)
DT	01-OCT-2000 (REMBLrel. 15, Last annotation update)
DE	CG14307 PROTEIN.
GN	CG14307.
OS	Drosophila melanogaster (Fruit fly).
OS	Euarysto; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
RESULT	15
09VB66	PRELIMINARY; PRT; 925 AA.
ID	09VC5; (REMBLrel. 15,保守性 10; 错配 13; 插入 3; 缺口 1;)
AC	09VE66; (REMBLrel. 13,保守性 10; 错配 13; 插入 3; 缺口 1;)
DT	01-MAY-2000 (REMBLrel. 13, Created)
DT	01-MAY-2000 (REMBLrel. 13, Last sequence update)
DT	01-MAY-2000 (REMBLrel. 13, Last annotation update)
DE	CG12964 PROTEIN.
GN	CG12964.
OS	Drosophila melanogaster (Fruit fly).
RESULT	16
09VB66	PRELIMINARY; PRT; 328 AA.
ID	09VC5; (REMBLrel. 15,保守性 10; 错配 13; 插入 3; 缺口 1;)
AC	09VE66; (REMBLrel. 13,保守性 10; 错配 13; 插入 3; 缺口 1;)
DT	01-MAY-2000 (REMBLrel. 13, Created)
DT	01-MAY-2000 (REMBLrel. 13, Last sequence update)
DT	01-MAY-2000 (REMBLrel. 13, Last annotation update)
DE	CG12964 PROTEIN.
GN	CG12964.
OS	Drosophila melanogaster (Fruit fly).

	Query	Match	Score	DB	Length	RA	OC
	SEQUENCE	FROM N.A.	11]	5	925	OR	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
RC	STRAIN=BERKELEY;					OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
	MEDLINE=2019e06; PubMed=10731132;					OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Adams M.D.,	Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,					OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,	Richardson S., Ashburner M., Henderson S.N.,					OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Sutton G.R., Lewin S.E., Yandell M.D., Zhang Q., Chen L.X.,	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,					OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Chapple M., Pfeiffer B.D.,	Branden R.C., Rogers Y.-H.C., Blazej R.G., Chapple M., Pfeiffer B.D.,					OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,	Abrial J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,					OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beesley E.M.,	Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beesley E.M.,					OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Beeson K.Y., Benches P.V., Bernheim B.P., Bhandari D., Bolshakov S.,	Beeson K.Y., Benches P.V., Bernheim B.P., Bhandari D., Bolshakov S.,					OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,					OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,	Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,					OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Cherry J.M., Cawley S., Dahake C., Davenport L.B., Davies P.,	Cherry J.M., Cawley S., Dahake C., Davenport L.B., Davies P.,					OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
de Pablo B., Deucher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,	de Pablo B., Deucher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,					OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Dodson K., Doupe L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,	Dodson K., Doupe L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,					OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Dubrin R.K.J., Evangelista C.C., Ferraz C., Ferreria S., Fleischmann W.,	Dubrin R.K.J., Evangelista C.C., Ferraz C., Ferreria S., Fleischmann W.,					OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Fosler C., Gabrielista A.E., Garg N.S., Geibart W.M., Glasser K.,	Fosler C., Gabrielista A.E., Garg N.S., Geibart W.M., Glasser K.,					OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Gloeckle A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,	Gloeckle A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,					OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,	Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,					OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Houston D., Houston K.A., Howland T.J., Wei M.-H., Illegwan C.,	Houston D., Houston K.A., Howland T.J., Wei M.-H., Illegwan C.,					OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Jelali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,	Jelali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,					OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,					OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Lasko P., Lei Y., Levitus A.A., Li J., Li Z., Liang Y., Lin X.,	Lasko P., Lei Y., Levitus A.A., Li J., Li Z., Liang Y., Lin X.,					OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,	Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,					OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Merkl S.M., Milashina N.V., Mobarry C., Morris J., Moskrafi A.,	Merkl S.M., Milashina N.V., Mobarry C., Morris J., Moskrafi A.,					OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,	Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,					OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacieb J.M.,	Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacieb J.M.,					OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Palazzolo M., Pittman G.S., Pan S., Pollard J.J., Puri V., Reese M.G.,	Palazzolo M., Pittman G.S., Pan S., Pollard J.J., Puri V., Reese M.G.,					OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,	Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,					OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,	Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,					OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Spieler E., Spradling A.C., Stapleton M., Strong R., Sun E.,	Spieler E., Spradling A.C., Stapleton M., Strong R., Sun E.,					OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Svirskas R., Tector C., Turner R., Venter E., Wang H., Wang X.,	Svirskas R., Tector C., Turner R., Venter E., Wang H., Wang X.,					OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissnenbach J.,	Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissnenbach J.,					OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,	Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,					OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao L.O., Zheng L.O.,	Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao L.O., Zheng L.O.,					OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Zheng X.H., Zhong F.N., Zhou W., Zhou X., Zhu S., Zhu X., Smith H.O.,	Zheng X.H., Zhong F.N., Zhou W., Zhou X., Zhu S., Zhu X., Smith H.O.,					OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,	Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,					OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
"The genome sequence of Drosophila melanogaster,"	"The genome sequence of Drosophila melanogaster,"					OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Science 287:2185-2195 (2000).	Science 287:2185-2195 (2000).					OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
EMAIL: AE033810; RA058133; DR052964;	EMAIL: AE033810; RA058133; DR052964;					OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
FLYBASE: FBgn00034022; CG12964;	FLYBASE: FBgn00034022; CG12964;					OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
SEQUENCE 925 AA; 10339 NW;	SEQUENCE 925 AA; 10339 NW;	60DAE21A15256284	CRC64;			OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Best Local Similarity 41.7%; Conservative 15;	Best Local Similarity 41.7%; Conservative 15;	Match	28.4%	Score	69.5;	DB	5;
Matches 8;	Mismatches 12;	Length 12;	Indels 1;	Gaps			
QY 2	439	0QFOECOONHQHQEORPEKKOCOVCRCREKQENP	37				

Query	Match	28 4 %;	Score	69.5;	DB	5;	Length
Best Local Similarity	41.7 %;	Pred.	No.	1. 3;			
Matches	15;	Conservative		8;	Mismatches	12;	Indels
Qy	2	QROFQBCQOCHHQFQRPERKQOCVRECRKYQENP	37				
Db	439	QQQHQYQQQHQHONHOAQQPAQ-QQQYOKPP	473				